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Query= SEQ ID NO:1
(3963 letters)

Sequences producing significant alignments:

Score E
(bits) Value

AC024258.9.1.160658
AL512429.14.1.11170
AC016395.5.1.166869

1794 0.0
1159 0.0
442 e-121

>AC024258.9.1.160658
Length = 160658

Score = 1794 bits (904), Expect = 0.0
Identities = 904/904 (100%)
Strand = Plus / Plus

Query: 1	atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat	60
Sbjct: 110106	atgcaagacgacagcatagaagcttctacttccatatctcagcttctaagagagagctat	110165
Query: 61	ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac	120
Sbjct: 110166	ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac	110225
Query: 121	ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt	180
Sbjct: 110226	ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt	110285
Query: 181	ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga	240
Sbjct: 110286	ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga	110345
Query: 241	ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaacgactt	300
Sbjct: 110346	ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaacgactt	110405
Query: 301	tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat	360
Sbjct: 110406	tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat	110465
Query: 361	aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat	420
Sbjct: 110466	aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat	110525
Query: 421	tgttctgaaacccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag	480
Sbjct: 110526	tgttctgaaacccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag	110585

Query: 481 ctatcctcccttttcaaattccacagctccaaaaggattagacctcgtgcctgcaaaaac 540
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 Sbjct: 110586 ctatcctcccttttcaaattccacagctccaaaaggattagacctcgtgcctgcaaaaac 110645

Query: 541 cacaagagtaaactggaatctcaaaacaaagttatgcaggaaaacagctccagtttctca 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110646 cacaagagtaaactggaatctcaaaacaaagttatgcaggaaaacagctccagtttctca 110705

Query: 601 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgaggataaccagg 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110706 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgaggataaccagg 110765

Query: 661 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 720
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 Sbjct: 110766 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 110825

Query: 721 gctgccagtgaggcggctggtggagacactacaccagggcttccccttcattctgtac 780
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 Sbjct: 110826 gctgccagtgaggcggctggtggagacactacaccagggcttccccttcattctgtac 110885

Query: 781 tatgaagaacctctggggcaacctccccggttcactcaaaagttacggagcagagaagtt 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110886 tatgaagaacctctggggcaacctccccggttcactcaaaagttacggagcagagaagtt 110945

Query: 841 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 110946 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 111005

Query: 901 aggt 904
 ||||
 Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0
 Identities = 372/375 (99%)
 Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcactcagccaactcyaccaccaacct 1658
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 154959 aggaaatgaggacctcagcaacaacgggtctcttcactcagccaactctaccaccaacct 155018

Query: 1659 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 1718
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 155019 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 155078

Query: 1719 ccccaaaccctcgagggggttctggtgaaccacaatgagccccgggtccagctccag 1778
|||||
Sbjct: 155079 ccccaaaccctcgagggggttctggtgaaccacaatgagccccgggtccagctccag 155138

Query: 1779 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 1838
|||||
Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggcccgattctttscaggagaggttcaa 1898
|||||
Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggcccgattctttccaggagaggttcaa 155258

Query: 1899 cggacaggcaacaaaaacccagagccttctttccccgtgaaagagccccctccagttct 1958
|||||
Sbjct: 155259 cggacaggcaacaaaaacccagagccttctttccccgtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973
|||||
Sbjct: 155319 ggccaaaccctaaact 155333

Score = 355 bits (179), Expect = 1e-94
Identities = 179/179 (100%)
Strand = Plus / Plus

Query: 901 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcggtccaggca 960
|||||
Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcggtccaggca 131664

Query: 961 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 1020
|||||
Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079
|||||
Sbjct: 131725 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 131783

Score = 286 bits (144), Expect = 9e-74
Identities = 144/144 (100%)
Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctgggtgtctttgaatgcagagtaa 1375
|||||
Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctgggtgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 1435
|||||
Sbjct: 147211 aaggagctccatctcctaagggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagatttttaggattttacagaaaa 1459
|||||
Sbjct: 147271 cagatttttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1482 agaggagatttgcaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 1541
|||||
Sbjct: 154367 agaggagatttgcaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 154426

Query: 1542 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 1601
|||||
Sbjct: 154427 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 154486

Score = 230 bits (116), Expect = 5e-57
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1130 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 1189
|||||
Sbjct: 137019 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 137078

Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcggtgtggcaaccatccagcag 1245
|||||
Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcggtgtggcaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 1302
|||||
Sbjct: 138704 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317
|||||
Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1077 aggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130
|||||
Sbjct: 134140 aggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 134193

Score = 48.1 bits (24), Expect = 0.041
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1460 aacctcgatccatggcagagccag 1483
|||||
Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170
Length = 11170

Score = 1159 bits (584), Expect = 0.0
Identities = 588/592 (99%)
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033
|||||
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttcctttcarcatgactgttttgaactccaa 2093
|||||
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttcctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccagcggtgacaacatccartaagcaggtgaaggctccttcacacagacgtt 2153
|||||
Sbjct: 4195 tgctccccagcggtgacaacatccagtaagcaggtgaaggctccttcacacagacgtt 4254

Query: 2154 cagcttggccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 2213
|||||
Sbjct: 4255 cagcttggccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 4314

Query: 2214 cccttcagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 2273
|||||
Sbjct: 4315 cccttcagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 4374

Query: 2274 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 2333
|||||
Sbjct: 4375 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 4434

Query: 2334 ttccatccaaaatgagccactcccaccaggcccaacagaaccracaccaccattcac 2393
|||||
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaaccaacaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453
|||||
Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaaccagtggtttctcagctctgttctgccttctctccc 2513
|||||
Sbjct: 4555 tcctaccagccggattcagaaccagtggtttctcagctctgttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatggrgctgcctagaagtgcaccatccatg 2565
|||||
Sbjct: 4615 tgccatcccacccacaaatgccatggggctgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 2565 gccatcccagggttagcggaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624
|||||
Sbjct: 5332 gccatcccagggttagcggaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataactttcagtga 2684
|||||
Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataactttcagtga 5451

Query: 2685 tgtcagaccaaaccagcagg 2704
|||||
Sbjct: 5452 tgtcagaccaaaccagcagg 5471

>AC016395.5.1.166869

Length = 166869

Score = 442 bits (223), Expect = e-121

Identities = 226/227 (99%)

Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760
|||||
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820
|||||
Sbjct: 157069 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880
|||||
Sbjct: 157009 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 156950

Query: 2881 ccagtcacattcacctgcaaaattgttgggatacctgttccaaaggt 2927
|||||
Sbjct: 156949 ccagttacattcacctgcaaaattgttgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113

Identities = 210/210 (100%)

Strand = Plus / Minus

Query: 3284 aggtgagtggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 3343
|||||
Sbjct: 146665 aggtgagtggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 146606

Query: 3344 cagatgcctcccacaagatgctgggtcagggagaccggagtcactctctgctcattgacc 3403
|||||
Sbjct: 146605 cagatgcctcccacaagatgctgggtcagggagaccggagtcactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaaaaaaccgggcaga 3463
|||||
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaaaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493
|||||
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 3852
|||||
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 3912
|||||
Sbjct: 135686 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 135627

Query: 3913 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963
|||||
Sbjct: 135626 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551
|||||
Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

Query: 3552 cgaaggccaccccgtgagactggagtgccgcgtgataggcatgccccacctgtgttcta 3611
|||||
Sbjct: 144144 cgaaggccaccccgtgagactggagtgccgcgtgataggcatgccccacctgtgttcta 144085

Query: 3612 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 3659
|||||
Sbjct: 144084 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 144037

Score = 306 bits (154), Expect = 9e-80
Identities = 158/159 (99%), Gaps = 1/159 (0%)
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983
|||||
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043
|||||
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551

Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081
|||||
Sbjct: 151550 gcaactacaccatcatggcagccaacccccagggtggaga 151512

Score = 272 bits (137), Expect = 1e-69
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 3657 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 3716
|||||
Sbjct: 139264 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 139205

Query: 3717 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 3776
|||||
Sbjct: 139204 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793
|||||
Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 3157 aggggaagatcccgagtgcaagaaagagacaaagagcccctacaggaacgctttttccga 3216
|||||
Sbjct: 148681 aggggaagatcccgagtgcaagaaagagacaaagagcccctacaggaacgctttttccga 148622

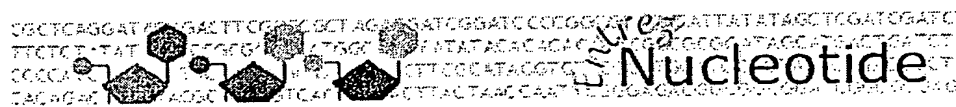
Query: 3217 ccacatttcctgcaggctcctggggataggttagctcatgaggggcgccctctgtcggctg 3276
|||||
Sbjct: 148621 ccacatttcctgcaggctcctggggataggttagctcatgaggggcgccctctgtcggctg 148562

Query: 3277 gactgtaaggt 3287
|||||
Sbjct: 148561 gactgtaaggt 148551

Score = 173 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Minus

Query: 3073 caggggagaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 3132
|||||
Sbjct: 150584 caggggagaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 150525

Query: 3133 ctaacctctgctgggtcagtctcacagg 3159
|||||||
Sbjct: 150524 ctaacctctgctgggtcagtctcacagg 150498



Boo

Clear

Details

Fe

Links

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61	ggtaactaca	gccttacgaa	atgtattttct	taataataaa	aacttgaaag	taaaaattac
121	tccttggtcc	tccagcagca	gaatggatgt	tgtattagca	ggcatgaaaa	cattaatctc
181	catgtatata	tccatctgag	ctctgagtgt	accagggtgca	ctgtcaataa	gcagcagtat
241	tttgaaagca	atctttttac	tgagcgggtg	gtctcaacag	tgggcttaag	cccatattaa
301	tattattcagt	acaccatgct	gtaaacagat	gagctgtcat	ccaggctttg	ttgttccatt
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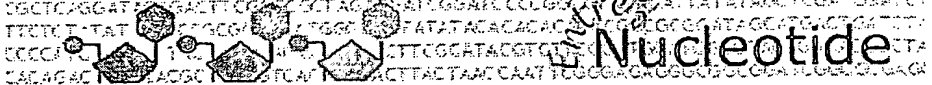
Nucleotide
 Protein
 Genome
 Structure
 PMC
 Taxonomy
 OMIM
 Boo

Search for
 Limits Preview/Index History Clipboard Details
 Display Show: Send to Get Subsequence Fe

☐ 1: AL512429. Human DNA sequenc...[gi:16508239]

Links

LOCUS AL512429 11170 bp DNA linear PRI 26-OCT-2001
 DEFINITION Human DNA sequence from clone RP11-429C3 on chromosome 10, complete sequence.
 ACCESSION AL512429
 VERSION AL512429.14 GI:16508239
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 11170)
 AUTHORS Mashreghi-Mohammadi, M.
 TITLE Direct Submission
 JOURNAL Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 COMMENT On Oct 29, 2001 this sequence version replaced gi:15028699. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10> RP11-429C3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-429C3 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-153K11 is at 9171 in this sequence.

  **Nucleotide**

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Bio

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Display Show:

☐ 1: AC016395. Homo sapiens chro...[gi:20564406]

Links

LOCUS AC016395 166869 bp DNA linear PRI 14-MAY-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-153K11, complete sequence.
ACCESSION AC016395
VERSION AC016395.5 GI:20564406
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 3 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 4 (bases 1 to 166869)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On May 14, 2002 this sequence version replaced gi:9929646.
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ORIGIN

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